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1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/520,946A

DATE: 06/21/2002

TIME: 14:46:47

Input Set : A:\Seqsub2.app

Output Set: N:\CRF3\06212002\H520946A.raw

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JUL 08 2002

SEQUENCE LISTING

TECH CENTER 1600/2900

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: BROW, MARY ANN D.

7 LYAMICHEV, VICTOR I.

8 OLIVE, DAVID M.

10 (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
11 PATHOGENS

13 (iii) NUMBER OF SEQUENCES: 165

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: MEDLEN & CARROLL

17 (B) STREET: 220 MONTGOMERY STREET, SUITE 2200

18 (C) CITY: SAN FRANCISCO

19 (D) STATE: CALIFORNIA

20 (E) COUNTRY: UNITED STATES OF AMERICA

21 (F) ZIP: 94104

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/08/520,946A

C--> 31 (B) FILING DATE: 30-Aug-1995

32 (C) CLASSIFICATION:

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: CARROLL, PETER G.

36 (B) REGISTRATION NUMBER: 32,837

37 (C) REFERENCE/DOCKET NUMBER: FORS-01756

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: (415) 705-8410

41 (B) TELEFAX: (415) 397-8338

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 2506 base pairs

48 (B) TYPE: nucleic acid

49 (C) STRANDEDNESS: double

50 (D) TOPOLOGY: linear

52 (ii) MOLECULE TYPE: DNA (genomic)

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

58	ATGAGGGGGA TGCTGCCCT CTTTGAGCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC	60
60	CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG	120
62	GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC	180
64	GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG	240

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66 TACAAGGCGG GCCGGGCCCC CACGCCGGAG GACTTTCCCC GGCAACTCGC CCTCATCAAG 300
68 GAGCTGGTGG ACCTCCTGGG GCTGGCGCGC CTCGAGGTCC CGGGCTACGA GGCGGACGAC 360
70 GTCCTGGCCA GCCTGGCCAA GAAGGCGGAA AAGGAGGGCT ACGAGGTCCG CATCCTCACC 420
72 GCCGACAAAG ACCTTTACCA GCTCCTTTCC GACCGCATCC ACGTCTCCA CCCCAGAGGG 480
74 TACCTCATCA CCCCAGCCTG GCTTTGGGAA AAGTACGGCC TGAGGCCCCA CCAGTGGGCC 540
76 GACTACCGGG CCCTGACCGG GGACGAGTCC GACAACCTTC CCGGGGTCAA GGGCATCGGG 600
78 GAGAAGACGG CGAGGAAGCT TCTGGAGGAG TGGGGGAGCC TGGAAGCCCT CCTCAAGAAC 660
80 CTGGACCGGC TGAAGCCCGC CATCCGGGAG AAGATCCTGG CCCACATGGA CGATCTGAAG 720
82 CTCTCCTGGG ACCTGGCCAA GGTGCGCACC GACCTGCCCC TGGAGGTGGA CTTGCGCCAA 780
84 AGGCGGGAGC CCGACCGGGA GAGGCTTAGG GCCTTTCTGG AGAGGCTTGA GTTTGGCAGC 840
86 CTCCTCCACG AGTTGGCCTT TCTGGAAAGC CCAAGGCCCT TGGAGGAGGC CCCCTGGCCC 900
88 CCGCCGGAAG GGGCCTTCGT GGGCTTTGTG CTTTCCCGCA AGGAGCCCAT GTGGGCCGAT 960
90 CTTCTGGCCC TGGCCGCCG CAGGGGGGGC CGGGTCCACC GGGCCCCCGA GCCTTATAAA 1020
92 GCCCTCAGGG ACCTGAAGGA GGCGCGGGGG GTTCTCGCCA AAGACCTGAG CGTTCTGGCC 1080
94 CTGAGGGAAG GCCTTGGCCT CCCGCCGGG GACGACCCCA TGCTCCTCGC CTACCTCCTG 1140
96 GACCCTTCCA ACACCAACCC CGAGGGGGTG GCCCGGCGCT ACGGCGGGGA GTGGACGGAG 1200
98 GAGGCGGGGG AGCGGGCCGC CTTTCCGAG AGGCTCTTCG CCAACCTGTG GGGGAGGCTT 1260
100 GAGGGGGAGG AGAGGCTCCT TTGGCTTTAC CGGGAGGTGG AGAGGCCCTT TTCCGCTGTC 1320
102 CTGGCCACA TGGAGGCCAC GGGGGTGC GC TGGACGTGG CCTATCTCAG GGCCTTGTC 1380
104 CTGGAGGTGG CCGAGGAGAT CGCCCGCCTC GAGGCCGAGG TCTTCCGCTT GGCCGGCCAC 1440
106 CCCTTCAACC TCAACTCCCG GGACAGCTG GAAAGGGTCC TCTTTGACGA GCTAGGGCTT 1500
108 CCCGCCATCG GCAAGACGGA GAAGACGGC AAGCGTCCA CCAGCGCCG CGTCTGGAG 1560
110 GCCCTCCGC CATCGTGAG AGGACCCACCATCGTGC AGTACCGGA GCTACCAAG 1620
112 CTGAAGAGCA CTTACATTGA CCCCTTGCCG GACCTCATCC ACCCAGGAC GGGCCGCTC 1680
114 CACACCCGCT TCAACCAGAC GGCCACGGCC ACGGCGAGG TAAGTAGCTC CGATCCCAAC 1740
116 CTCCAGAACA TCCCGTCCG CACCCGCTT GGGCAGAGGA TCCGCCGGC CTTTCATCGCC 1800
118 GAGGAGGGGT GGTATTGGT GGCCCTGGAC TATAGCCAGA TAGAGCTCAG GGTGCTGGCC 1860
120 CACCTCTCCG GCGACGAGAA CCTGATCCG GTCTTCCAG AGGGGCGGGA CATCCACAG 1920
122 GAGACGCCCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCG TGGACCCCTT GATGCGCCG 1980
124 GCGGCCAAGA CCATCAACTT CGGGGTCTCT TACGGCATGT CGGCCACCG CCTCTCCAG 2040
126 GAGCTAGCCA TCCCTTACGA GGAGGCCAG GCCTTCATTG AGCGTACTT TCAGAGCTTC 2100
128 CCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG GGGGTACGTG 2160
130 GAGACCTCT TCGCCGCCG CCGCTACGT CCAGACCTAG AGGCCCGGT GAAGAGCGTG 2220
132 CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCGTCC AGGGCACCGC CGCCGACCTC 2280
134 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGC CAGGATGCTC 2340
136 CTTAGGTCC ACGACGAGCT GGTCCTCGAG GCCCCAAAAG AGAGGGCGGA GGCCGTGGCC 2400
138 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCTT GGAGGTGGAG 2460
140 GTGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC 2506
142 (2) INFORMATION FOR SEQ ID NO: 2:
144 (i) SEQUENCE CHARACTERISTICS:
145 (A) LENGTH: 2496 base pairs
146 (B) TYPE: nucleic acid
147 (C) STRANDEDNESS: double
148 (D) TOPOLOGY: linear
150 (ii) MOLECULE TYPE: DNA (genomic)
154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
156 ATGGCGATGC TTCCCTCTT TGAGCCCAA GGCCGCGTGC TCCTGGTGGA CGGCCACCAC 60
158 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTACCA CCAGCCGCGG CGAACCCGTT 120
160 CAGGCGGTCT ACGGCTTCG CAAAAGCCTC CTAAGGCCCT TGAAGGAGGA CGGGGACGTG 180

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162	GTGGTGGTGG	TCTTTGACGC	CAAGGCCCCC	TCCTTCCGCC	ACGAGGCCTA	CGAGGCCTAC	240
164	AAGGCGGGCC	GGGCCCCCAC	CCCGGAGGAC	TTTCCCCGGC	AGCTGGCCCT	CATCAAGGAG	300
166	TTGGTGGACC	TCCTAGGCCT	TGTGCGGCTG	GAGGTTCCCC	GCTTTGAGGC	GGACGACGTG	360
168	CTGGCCACCC	TGGCCAAGCG	GGCGGAAAAG	GAGGGGTACG	AGGTGCGCAT	CCTCACTGCC	420
170	GACCGCGACC	TCTACCAGCT	CCTTTCGGAG	CGCATCGCCA	TCCTCCACCC	TGAGGGGTAC	480
172	CTGATCACCC	CGGCGTGGCT	TTACGAGAAG	TACGGCCTGC	GCCCGGAGCA	GTGGGTGGAC	540
174	TACCGGGCCC	TGGCGGGGGA	CCCCCTCGAT	AACATCCCCG	GGGTGAAGGG	CATCGGGGAG	600
176	AAGACCGCCC	AGAGGCTCAT	CCGCGAGTGG	GGGAGCCTGG	AAAACCTCTT	CCAGCACCTG	660
178	GACCAAGTGA	AGCCCTCCTT	GCGGGAGAAG	CTCCAGGCGG	GCACTGGAGG	CCTGGCCCTT	720
180	TCCCGGAAGC	TTTCCCAGGT	GCACACTGAC	CTGCCCCTGG	AGGTGGACTT	CGGGAGGCGC	780
182	CGCACACCCA	ACCTGGAGGG	TCTGCGGGCT	TTTTTGGAGC	GGTTGGAGTT	TGGAAGCCTC	840
184	CTCCACGAGT	TCGGCCTCCT	GGAGGGGCGG	AAGGCGGCAG	AGGAGGCCCC	CTGGCCCCCT	900
186	CCGGAAGGGG	CTTTTTTGGG	CTTTTCCTTT	TCCCGTCCCG	AGCCCATGTG	GGCCGAGCTT	960
188	CTGGCCCTGG	CTGGGGCGTG	GGAGGGGCGC	CTCCATCGGG	CACAAGACCC	CCTTAGGGGC	1020
190	CTGAGGGACC	TTAAGGGGGT	GCGGGGAATC	CTGGCCAAGG	ACCTGGCGGT	TTTGGCCCTG	1080
192	CGGGAGGGCC	TGGACCTCTT	CCCAGAGGAA	GACCCCATGC	TCCTGGCCTA	CCTTCTGGAC	1140
194	CCCTCCAACA	GACCCCTGTA	GGGGGTGGCC	CGGCGTTACG	GGGGGGAGTG	GACGGAGGAT	1200
196	GCGGGGGAGA	GGGCCCTCCT	GGCCGAGCGC	CTCTTCCAGA	CCCTAAAGGA	GCGCCTTAAG	1260
198	GGAGAAGAAC	GCCTGCTTTG	GCTTTACGAG	GAGGTGGAGA	AGCCGCTTTC	CCGGGTGTTG	1320
200	GCCCGGATGG	AGGCCACGGG	GGTCCGGCTG	GACGTGGCCT	ACCTCCAGGC	CCTCTCCCTG	1380
202	GAGGTGGAGG	CGGAGGTGCG	CCAGCTGGAG	GAGGAGGTCT	TCCGCTGGC	CGGCCACCCC	1440
204	TTCAACCTCA	ACTCCCGCGA	CCAGCTGGAG	CGGGTGCTCT	TTGACGAGCT	GGGCTGCCT	1500
206	GCCATCGGCA	AGACGGAGAA	GACGGGGAAA	CGCTCCACCA	GCGCTGCCGT	GCTGGAGGCC	1560
208	CTGCGAGAGG	CCCACCCCAT	CGTGGACCGC	ATCCTGCAGT	ACCGGGAGCT	CACCAAGCTC	1620
210	AAGAACACCT	ACATAGACCC	CCTGCCCGCC	CTGGTCCACC	CCAAGACCGG	CCGGCTCCAC	1680
212	ACCCGCTTCA	ACCAGACGGC	CACCGCCACG	GGCAGGCTTT	CCAGCTCCGA	CCCCAACCTG	1740
214	CAGAACATCC	CCGTGCGCAC	CCCTCTGGGC	CAGCGCATCC	GCCGAGCCTT	CGTGGCCGAG	1800
216	GAGGGCTGGG	TGCTGGTGGT	CTTGGACTAC	AGCCAGATTG	AGCTTCGGGT	CCTGGCCCCAC	1860
218	CTCTCCGGGG	ACGAGAACCT	GATCCGGGTC	TTTCAGGAGG	GGAGGGACAT	CCACACCCAG	1920
220	ACCGCCAGCT	GGATGTTTCG	CGTTTTCCCC	GAAGGGGTAG	ACCCTCTGAT	GCGCCGGGCG	1980
222	GCCAAGACCA	TCAACTTCGG	GGTGCTCTAC	GGCATGTCCG	CCCACCGCCT	CTCCGGGGAG	2040
224	CTTTCCATCC	CCTACGAGGA	GGCGGTGGCC	TTCATTGAGC	GCTACTTCCA	GAGCTACCCC	2100
226	AAGGTGCGGG	CCTGGATTGA	GGGGACCCTC	GAGGAGGGCC	GCCGGCGGGG	GTATGTGGAG	2160
228	ACCCTCTTCG	GCCGCCGGCG	CTATGTGCCC	GACCTCAACG	CCCAGGTGAA	GAGCGTGCGC	2220
230	GAGGCGGCGG	AGCGCATGGC	CTTCAACATG	CCGTTCCAGG	GCACCGCCGC	CGACCTCATG	2280
232	AAGCTGGCCA	TGGTGCGGCT	TTTCCCCCGG	CTTCAGGAAC	TGGGGGCGAG	GATGCTTTTG	2340
234	CAGGTGCACG	ACGAGCTGGT	CCTCGAGGCC	CCCAAGGACC	GGGCGGAGAG	GGTAGCCGCT	2400
236	TTGGCCAAGG	AGGTATGGA	GGGGGTCTGG	CCCTGCAGG	TGCCCTGGA	GGTGGAGGTG	2460
238	GGCCTGGGGG	AGGACTGGCT	CTCCGCCAAG	GAGTAG			2496
240	(2) INFORMATION FOR SEQ ID NO: 3:						
242	(i) SEQUENCE CHARACTERISTICS:						
243	(A) LENGTH: 2504 base pairs						
244	(B) TYPE: nucleic acid						
245	(C) STRANDEDNESS: double						
246	(D) TOPOLOGY: linear						
248	(ii) MOLECULE TYPE: DNA (genomic)						
252	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:						
254	ATGGAGGCGA	TGCTTCCGCT	CTTTGAACCC	AAAGGCCGGG	TCCTCCTGGT	GGACGGCCAC	60
256	CACCTGGCCT	ACCGCACCTT	CTTCGCCCTG	AAGGGCCTCA	CCACGAGCCG	GGGCGAACCG	120

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258	GTGCAGGCGG	TCTACGGCTT	CGCCAAGAGC	CTCCTCAAGG	CCCTGAAGGA	GGACGGGTAC	180
260	AAGGCCGTCT	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGAG	240
262	GCCTACAAGG	CGGGGAGGGC	CCCGACCCCC	GAGGACTTCC	CCCGGCAGCT	CGCCCTCATC	300
264	AAGGAGCTGG	TGGACCTCCT	GGGGTTTACC	CGCCTCGAGG	TCCCCGGCTA	CGAGGCGGAC	360
266	GACGTTCTCG	CCACCTGGC	CAAGAAGGCG	GAAAAGGAGG	GGTACGAGGT	GCGCATCCTC	420
268	ACCGCCGACC	GCGACCTCTA	CCAACCTCGT	TCCGACCGCG	TCGCCGTCTT	CCACCCCGAG	480
270	GGCCACCTCA	TCACCCCGGA	GTGGCTTTGG	GAGAAGTACG	GCCTCAGGCC	GGAGCAGTGG	540
272	GTGGACTTCC	GCGCCCTCGT	GGGGGACCCC	TCCGACAACC	TCCCCGGGGT	CAAGGGCATC	600
274	GGGGAGAAGA	CCGCCCTCAA	GCTCCTCAAG	GAGTGGGGAA	GCCTGGAAAA	CCTCCTCAAG	660
276	AACCTGGACC	GGGTAAAGCC	AGAAAACGTC	CGGGAGAAGA	TCAAGGCCCA	CCTGGAAGAC	720
278	CTCAGGCTCT	CCTTGAGCT	CTCCCGGGTG	CGCACCGACC	TCCCCCTGGA	GGTGGACCTC	780
280	GCCCAGGGGC	GGGAGCCCGA	CCGGGAGGGG	CTTAGGGCCT	TCCTGGAGAG	GCTGGAGTTC	840
282	GGCAGCCTCC	TCCACGAGTT	CGGCCTCCTG	GAGGCCCCCG	CCCCCCTGGA	GGAGGCCCCC	900
284	TGGCCCCCGC	CGGAAGGGGC	CTTCGTGGGC	TTCGTCTCT	CCCGCCCCGA	GCCCATGTGG	960
286	GCGGAGCTTA	AAGCCCTGGC	CGCCTGCAGG	GACGGCCGGG	TGCACCGGGC	AGCAGACCCC	1020
288	TTGGCGGGGC	TAAAGGACCT	CAAGGAGGTC	CGGGGCCCTC	TCGCCAAGGA	CCTCGCCGTC	1080
290	TTGGCCTCGA	GGGAGGGGCT	AGACCTCGTG	CCCGGGGACG	ACCCCATGCT	CCTCGCCTAC	1140
292	CTCCTGGACC	CCTCCAACAC	CACCCCGCAG	GGGGTGGCGC	GGCGCTACGG	GGGGGAGTGG	1200
294	ACGGAGGACG	CCGCCACCG	GGCCCTCCTC	TCGGAGAGGC	TCCATCGGAA	CCTCCTTAAG	1260
296	CGCCTCGAGG	GGGAGGAGAA	GCTCCTTTGG	CTCTACCACG	AGGTGGAAAA	GCCCCCTCTC	1320
298	CGGGTCCTGG	CCCACATGGA	GGCCACCGGG	GTACGGCTGG	ACGTGGCCTA	CCTTCAGGCC	1380
300	CTTTCCTTGG	AGCTTGCGGA	GGAGATCCGC	CGCCTCGAGG	AGGAGGTCTT	CCGCTTGGCG	1440
302	GGCCACCCCT	TCAACCTCAA	CTCCCGGGAC	CAGCTGGAAA	GGGTGCTCTT	TGACGAGCTT	1500
304	AGGCTTCCCG	CCTTGGGGAA	GACGCAAAAG	ACAGGCAAGC	GCTCCACCAG	CGCCGCGGTG	1560
306	CTGGAGGCC	TACGGGAGGC	CCACCCCATC	GTGGAGAAGA	TCCTCCAGCA	CCGGGAGCTC	1620
308	ACCAAGCTCA	AGAACACCTA	CGTGGACCCC	CTCCCAAGCC	TCGTCCACCC	GAGGACGGGC	1680
310	CGCCTCCACA	CCCGCTTCAA	CCAGACGGCC	ACGGCCACGG	GGAGGCTTAG	TAGCTCCGAC	1740
312	CCCAACCTGC	AGAACATCCC	CGTCCGCACC	CCCTTGGGCC	AGAGGATCCG	CCGGGCCTTC	1800
314	GTGGCCGAGG	CGGGTTGGGC	GTTGGTGGCC	CTGGACTATA	GCCAGATAGA	GCTCCGCGTC	1860
316	CTCGCCACCC	TCTCCGGGGA	CGAAAACCTG	ATCAGGGTCT	TCCAGGAGGG	GAAGGACATC	1920
318	CACACCCAGA	CCGCAAGCTG	GATGTTCCGC	GTCCCCCGCG	AGGCCGTGGA	CCCCCTGATG	1980
320	CGCCGGGCGG	CCAAGACGGT	GAACTTCGGC	GTCTCTACG	GCTGTCCGC	CCATAGGCTC	2040
322	TCCCAGGAGC	TTGCCATCCC	CTACGAGGAG	GCGGTGGCCT	TTATAGAGGC	TACTTCCAAA	2100
324	GCTTCCCCAA	GGTGCGGGCC	TGGATAGAAA	AGACCCTGGA	GGAGGGGAGG	AAGCGGGGCT	2160
326	ACGTGGA AAC	CCTCTTCGGA	AGAAGGCGCT	ACGTGCCCCG	CCTCAACGCC	CGGGTGAAGA	2220
328	GCGTCAGGGA	GGCCGCGGAG	CGCATGGCCT	TCAACATGCC	CGTCCAGGGC	ACCGCCGCCG	2280
330	ACCTCATGAA	GCTCGCCATG	GTGAAGCTCT	TCCCCCGCCT	CCGGGAGATG	GGGGCCCGCA	2340
332	TGCTCCTCCA	GGTCCACGAC	GAGCTCCTCC	TGGAGGCCCC	CCAAGCGCGG	GCCGAGGAGG	2400
334	TGGCGGCTTT	GGCCAAGGAG	GCCATGGAGA	AGGCCTATCC	CCTCGCCGTG	CCCCTGGAGG	2460
336	TGGAGGTGGG	GATGGGGGAG	GACTGGCTTT	CCGCCAAGGG	TTAG		2504

338 (2) INFORMATION FOR SEQ ID NO: 4:

340 (i) SEQUENCE CHARACTERISTICS:

341 (A) LENGTH: 832 amino acids

342 (B) TYPE: amino acid

343 (C) STRANDEDNESS: single

344 (D) TOPOLOGY: linear

346 (ii) MOLECULE TYPE: protein

350 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

352 Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu

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353      1              5              10              15
355  Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly
356              20              25              30
358  Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
359              35              40              45
361  Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
362              50              55              60
364  Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
365  65              70              75              80
367  Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
368              85              90              95
370  Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
371              100              105              110
373  Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
374              115              120              125
376  Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
377  130              135              140
379  Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
380  145              150              155              160
382  Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
383              165              170              175
385  Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
386              180              185              190
388  Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
389              195              200              205
391  Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
392  210              215              220
394  Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
395  225              230              235              240
397  Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
398              245              250              255
400  Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
401              260              265              270
403  Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
404              275              280              285
406  Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
407  290              295              300
409  Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
410  305              310              315              320
412  Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro
413              325              330              335
415  Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
416              340              345              350
418  Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro
419              355              360              365
421  Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
422  370              375              380
424  Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
425  385              390              395              400

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/08/520,946A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 4,5,181,182,190,366,617,628,685,714,722,738,784,1022,1029
Seq#:7; N Pos. 1038,1053,1098,1105,1206,1227,1244,1251,1252,1253,1350,1380
Seq#:7; N Pos. 1497,1530,1569,1572,1641,1653,1655,1770,1812,2319,2346,2396
Seq#:8; Xaa Pos.2,63,109,186,205,209,227,228,233,240,243,244,247,260,290
Seq#:8; Xaa Pos.329,336,340,368,414,417,418,431,551,605,773,794,798,823,833

VERIFICATION SUMMARY

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Input Set : A:\Seqsub2.app

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:1135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:48
L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:96
L:1159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:176
L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:192
L:1165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:208
L:1168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:224
L:1171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:240
L:1174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:256
L:1180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:288
L:1186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:320
L:1189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:336
L:1192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:352
L:1201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:400
L:1204 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:416
L:1228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:544
L:1237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:592
L:1270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:768
L:1273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:784
L:1279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:816
L:1282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:832